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Targeting Cultivars onto Rice Growing Environments Using AMMI and SREG GGE Biplot Analyses

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ABSTRACT

The identification of the highest yielding cultivar for a specific environment on the basis of both genotype (G) and genotype × environment (GE) interaction would be useful to breeders and producers since yield estimates based only on G and environment (E) effects are insufficient. The objective of this study was to demonstrate the usefulness of additive main effects and multiplicative interactions (AMMI) model analysis and G plus GE interaction (GGE) biplots, obtained from sites regression (SREG) model analysis in interpreting GE grain yield data. Replicated grain yield data of six rice (*Oryza sativa* L.) cultivars (Cocodrie, Cypress, Jefferson, Lemont, Saber, and Wells) from three main cropping seasons (2000, 2001, and 2002) at four locations in Texas, USA (Bay City, Eagle Lake, Ganado, and Beaumont) were obtained and used for this purpose. Through AMMI model analysis, the magnitude and significance of the effects of GE interaction and its interaction principal components relative to the effects of G and E were estimated. The stability and adaptability of specific cultivars were assessed by plotting their nominal grain yields at specific environments in an AMMI biplot, which aided in the identification of megaenvironments (environments with the same highest yielding cultivar). Appropriate check cultivars for all locations or for specific locations were identified. Through GGE biplots of SREG model analysis results, the relative yield performance of cultivars at a specific environment were illustrated, the performance of a cultivar at different environments was compared, the performance of two cultivars at different environments were compared, the highest yielding cultivars at the different megaenvironments were identified, and ideal cultivars and test locations were identified.

Genotype × environment interaction is commonly observed by crop producers and breeders as the differential ranking of cultivar yields among locations or years. Plant breeders conduct multiple-environment trials (MET) primarily to identify the superior cultivar for a target region and secondarily to determine if the target region can be subdivided into different megaenvironments (Yan et al., 2000). The targeting of cultivars to specific locations is difficult when GE interaction is present, since yield is less predictable and cannot be interpreted based only on G and E means (Ebdon and Gauch, 2002a).

Zobel et al. (1988) compared the traditional statistical analyses (analysis of variance [ANOVA], principal component analysis [PCA], and linear regression) with AMMI analyses, and showed that the traditional analyses were not always effective in analyzing the MET data structure. The ANOVA is an additive model that describes main effects effectively and determines if GE interaction is a significant source of variation, but it does not provide insight into the patterns of genotypes or environments that give rise to the interaction. The PCA is a multiplicative model that contains no sources of variation for additive G or E main effects and does not analyze the interactions effectively. The linear regression method uses E means, which are frequently a poor estimate of environments, such that the fitted lines in most cases account for a small fraction of the total GE (Zobel et al., 1988). The AMMI model analysis combines the ANOVA (with additive parameters) and PCA (with multiplicative parameters) into a single analysis. The AMMI model analysis is useful in making cultivar recommendations, specifically by megaenvironment analysis, in which the best performing cultivar for each subregion of the crop's growing region is identified (Zobel et al., 1988; Gauch and Zobel, 1997). Gauch and Zobel (1997) demonstrated the usefulness of AMMI analysis in supporting breeding program decisions, such as in the selection of environments or test site locations. Although AMMI model analysis results are based only on yield data (not environmental data), Ebdon and Gauch (2002a) reported that AMMI environmental (interaction) statistics were correlated with environmental factors, such as precipitation, mean daily maximum and minimum temperature, altitude, latitude, N fertilization, irrigation, and clay content.

Biplot graphs, which show markers of both genotypes and environments, are used to present AMMI analysis results (Gauch and Zobel, 1997; Ebdon and Gauch, 2002b). Recently, biplots have also been used to interpret results of the SREG model analysis of MET data. Genotype and GE interaction, which are the two factors that are important in cultivar selection, are the sources of variation in the SREG model analysis of MET data. These factors are graphically shown through a GGE biplot, which is used in the visual evaluation of both genotypes and environments (Yan et al., 2000, 2001; Yan and Hunt, 2002).

Crop breeding programs should take GE interaction into consideration and have an estimate of its magnitude, relative to the magnitude of G and E effects, which affect grain yield. Furthermore, the identification of the cultivar that yields best at a specific growing environment would be useful to breeders and producers. Using

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Abbreviations: AMMI, additive main effects and multiplicative interactions; E, environment; G, genotype; GE, genotype × environment; GEI, genotype environment interaction; GGE, genotype and genotype × environment; IPCA, interaction principal component analysis; MET, multiple-environment trial; PCA, principal component analysis; SREG, sites regression; SVD, singular value decomposition.

data from a multienvironment (years and locations) experiment, this study demonstrated the utility of AMMI model analysis and GGE biplots obtained from SREG model analysis in evaluating the significance and magnitude of the GE interaction effect on grain yield and in determining the best performing cultivar for each environment.

MATERIALS AND METHODS

Experimental Data

Six semidwarf, long-grain rice cultivars that represented the major cultivars grown in commercial fields in Texas were used in this study. They were Cocodrie (Linscombe et al., 2000), Cypress (Linscombe et al., 1993), Jefferson (McClung et al., 1997), Lemont (Bollich et al., 1985), Saber (McClung et al., 2004), and Wells (Moldenhauer et al., 2000). Yield potential of these cultivars ranges from high (Wells) to good (other cultivars), milling quality ranges from excellent (Saber and Cyress) to average (Wells), and maturity ranges from very short (Jefferson) to mid-season (Cypress, Lemont, and Saber) (Wilson et al., 2003)

Replicated grain yield data (kg ha^{-1}) were obtained during three main cropping seasons (2000, 2001, and 2002) from four locations in Texas (Bay City, Matagorda County, 28°58′ N, 95°57′ W; Eagle Lake, Colorado County, 29°35′ N, 96°20′ W; Ganado, Jackson County, 28°59′ N, 96° 27′ W; and Beaumont, Jefferson County, 29°57′ N, 94°30′ W). The randomized complete block design was used in all locations and years. At Bay City, the numbers of replicates were two, four, and three in 2000, 2001, and 2002, respectively. At Eagle Lake and Ganado, there were three replicates in 2000 and 2002, and four replicates in 2001. There were eight replicates at Beaumont in each of the 3 yr. Plot dimensions during the 2000, 2001, and 2002 field experiments were 1.9 × 4.9 m at Bay City, 1.2 × 6.1 m at Beaumont, and 1.9 × 4.9 m at Ganado. At Eagle Lake, they were 1.9 × 4.9 m in 2000 and 2001, and 1.5 × 6.1 m in 2002. Planting dates were 19 April 2000, 1 May 2001, and 17 April 2002 at Bay City; 20 April 2000, 27 April 2001, and 5 April 2002 at Beaumont; 27 March 2000, 9 April 2001, and 5 April 2002 at Eagle Lake; and 6 April 2000, 5 April 2001, and April 3 2002 at Ganado.

Nitrogen, P, and K were added as fertilizer in the amounts of 177–43–43, 199–43–43, and 244–43–43 kg ha^{-1} at Bay City in 2000, 2001, and 2002, respectively. At Beaumont, 224 kg ha^{-1} of N was added as fertilizer in 2000, 2001, and 2002, respectively, while 56 kg ha^{-1} P was added in 2002. The amounts of N, P, and K added as fertilizer at Eagle Lake in 2000, 2001, and 2002 were 224–43–43, 231–43–43, and 155–43–43 kg ha^{-1}, respectively. At Ganado, fertilizer N, P, and K were added in the amounts of 222–43–43, 231–43–43, and 222–43–43 kg ha^{-1} in 2000, 2001, and 2002, respectively. Insect pest, disease, and weed management practices were applied as outbreak preventive measures.

Additive Main Effects and Multiplicative Interaction Model Analysis

The AMMI model analysis of grain yield was performed by a SAS (SAS Institute Inc., 1999) program written by Hernandez and Crossa (2000). Although the number of replications varied across locations and years (from two to eight replications), only two randomly selected replications were used because of the requirement of equal replications by the SAS program. In the analysis, each combination between the four locations and 3 yr was considered as an environment, making a total of 12 environments. The ANOVA model is

$$Y_{ger} = \mu + \alpha_g + \beta_e + \theta_{ge} + \varepsilon_{ger},$$

and the AMMI model is

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_{n-1}^{N} \lambda_n \zeta_{gn} \eta_{en} + \rho_{ge} + \varepsilon_{ger},$$

where Y_{ger} is the grain yield of genotype g in environment e for replicate r, μ is the grand mean, α_g are genotype mean deviations (mean minus the grand mean), β_e are the environment mean deviations, N is the number of SVD (singular value decomposition) axes retained in the model, λ_n is the singular value for SVD axis n, ζ_{gn} are the genotype singular vector values for SVD axis $\boldsymbol{n}$, η_{en} are the environment singular vector values for SVD axis n, θ_{ge} are the interaction residuals, ρ_{ge} are the AMMI residuals, and ε_{ger} is the error term.

Correlation Analyses

Correlation analyses were conducted to determine if any linear relationship existed between AMMI environment interaction principal components analysis (IPCA) axis scores and environmental variables. The 29 variables were amounts of N, P, and K applied during fertilization, soil pH, latitude, longitude, dates of growth stages (seedling emergence date, heading, and harvest), and climatic data (temperature [maximum, minimum, and daily mean], heat units [sum of degree days > 10°C and average daily degree days > 10°C)], daily mean relative humidity, heat index [maximum, minimum, daily mean], and precipitation). Climatic data for the entire growing season (emergence to maturity) and for the period from heading to maturity were tested for their correlation with environment IPCA scores. The weather data of each location and year was obtained from a weather station at or near the experimental site.

AMMI Biplot Analyses

The results of the AMMI model analysis were interpreted on the basis of two AMMI biplots—a biplot that showed the main and first interaction principal components analysis (IPCA 1) axis effects of both G and E and a biplot that showed the nominal yield (expected yield from the AMMI model equation without environmental deviations) of genotypes across IPCA 1 scores (Gauch and Zobel, 1997). The nominal grain yield of each genotype was estimated as the G mean plus the product of G and E IPCA 1 scores.

Sites Regression Model Analysis

The SREG model analysis of grain yield was performed by a SAS (SAS Institute Inc., 1999) program written by Burgueño et al. (2001). The SREG linear-bilinear model is represented by

$$\bar{y}_{ij.} = \mu + \delta_j + \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} + \bar{\varepsilon}_{ij.}$$

where $\bar{y}_{ij.}$ is the mean of the ith cultivar in the jth environment for g genotypes and e environments (i = 1, 2, …, g and j = 1, 2, …, e); μ is the overall mean; δ_j is the site effect; λ_k ($\lambda_1 \geq \lambda_2 \geq \ldots \geq \lambda_t$) are scaling constants (singular values) that allow the imposition of orthonormality constraints on the singular vectors for cultivars, $\alpha_k = (\alpha_{1k},\ldots,\alpha_{gk})$ and sites, $\gamma_k = (\gamma_{1k},\ldots,\gamma_{ek})$; α_{ik} and γ_{jk} for k = 1, 2, 3, … are called "primary," "secondary," "tertiary," … etc. effects of the ith cultivar and jth site, respectively; $\bar{\varepsilon}_{ij.}$ is the residual error assumed to be normally and

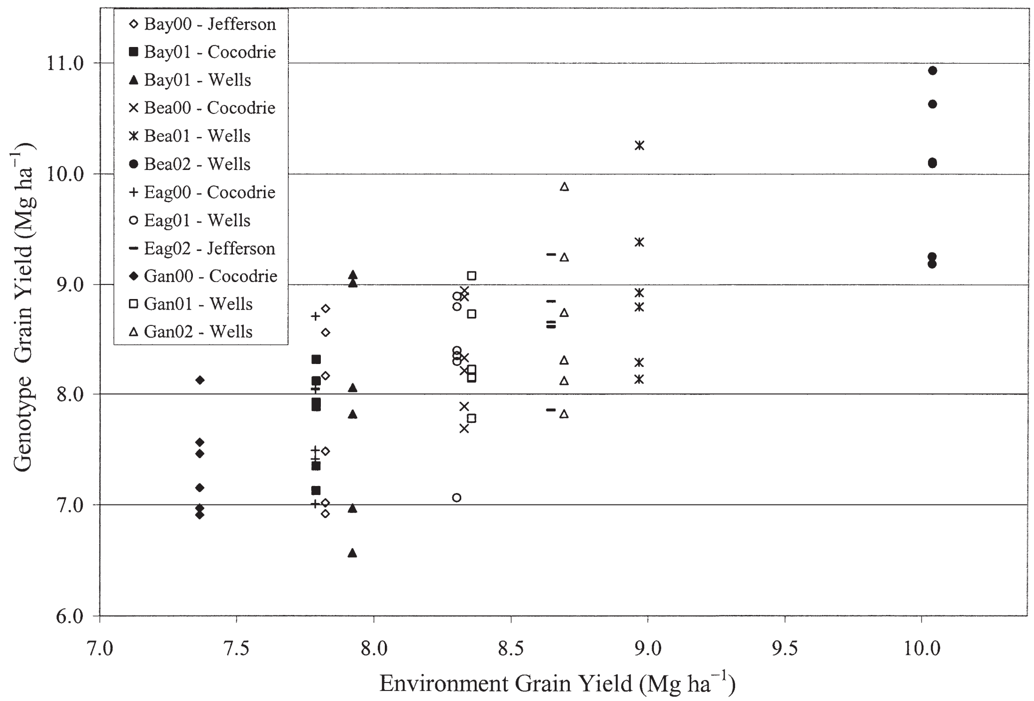

Fig. 1. Grain yield of six rice cultivars grown at four locations for 3 yr. The highest yielding cultivar in each environment is indicated. Abbreviations: Bay–Bay City, Bea–Beaumont, Eag–Eagle Lake, Gan–Ganado, 00–2000, 01–2001, 02–2002.

independently distributed (0, σ^2/r) (where σ^2 is the pooled error variance and r is the number of replicates). In the SREG model, the main effects of cultivars (G) plus the GE interaction were absorbed into the bilinear terms (Burgueño et al., 2001; Crossa et al., 2002).

GGE Biplot Analyses

The GGE biplot methodology, which is composed of two concepts, the biplot concept (Gabriel, 1971) and GGE concept (Gauch and Zobel 1996; Yan et al., 2000), was used to visually analyze the results of SREG analysis of MET data. This methodology uses a biplot to show the two factors (G plus GE) that are important in cultivar evaluation and that are also the sources of variation in SREG model analysis of MET data (Yan et al., 2000, 2001). The GGE biplot shows the first two principal components (PC1 and PC2, also referred to as primary and secondary effects, respectively) derived from subjecting environment-centered yield data (the yield variation due to GGE) to singular value decomposition (Yan et al., 2000). In this study, GGE biplots were used to compare the performance of different genotypes at an environment, compare the performance of a genotype at different environments, compare the performance of two genotypes at all environments, identify the highest yielding genotypes at the different megaenvironments, and identify ideal cultivars and test locations.

RESULTS AND DISCUSSION

Crossover GE Interaction

An indication of the presence of GE interaction is the differential yield ranking of cultivars across environments. In this study, different cultivars produced the highest grain yields at different environments. Wells was the highest yielding cultivar at six environments, Cocodrie was highest at four environments, and Jefferson was highest at two environments (Fig. 1). Wells was the highest yielder (10.93 Mg ha^{-1}) at the highest yielding environment (Beaumont in 2002), while Cocodrie was the highest yielder (8.13 Mg ha^{-1}) at the lowest yielding environment (Ganado in 2000).

AMMI Model Analysis

The ANOVA showed that rice grain yields were significantly affected by E and G, which explained 55.4 and 17.8% of the G + E + GE variation, respectively (Table 1). Environment grain yields (averaged across cultivars) ranged from 7.36 Mg ha^{-1} at Ganado in 2000 to 10.03 Mg ha^{-1} at Beaumont in 2002. Cultivar grain yields (averaged across environments) ranged from 7.96 Mg ha^{-1} for Saber to 8.88 Mg ha^{-1} for Cocodrie. Genotype $\times$ environment interaction significantly explained 26.7% of the G + E + GE variation in grain yield. The partitioning of GE interaction through AMMI model analysis showed IPCA 1 and IPCA 2 were significant factors that explained 40.9% and 27.0% of GE sum of squares (SS), respectively (Table 1). Together, they accounted for 67.9% of GE interaction SS. The third IPCA explained 22.2% of GE SS, but this was not significant. In comparison, Gauch and Zobel (1996) reported that in normal METs, E accounts for 80% of the total yield variation, while G and GE each account for about 10%.

Relationship between Environment IPCA Scores and Environment Variables

Among the 29 environmental variables tested for their correlation with IPCA 1, IPCA 2, or IPCA 3, only mean minimum heat index was significantly correlated with E IPCA 1 ($r = -0.618$, P value = 0.0324). Environments with higher IPCA 1 scores would be environ-

Table 1. AMMI† analysis of variance for the significance of the effects of genotype, environment, genotype × environment interaction (GEI) on grain yield, and the partitioning of GEI into AMMI axes.

Source of Variation	df	SS	MS	*F* value	*P* value	Percentage of GEI SS	Cumulative percentage of GEI SS
Block	1	0.049	0.049	0.144	0.7055		
Environment	11	65.795	5.981	17.654	<0.0001		
Genotype	5	21.174	4.235	12.499	<0.0001		
GEI	55	31.733	0.577	1.703	0.0182		
IPCA 1	15	12.980	0.865	2.554	0.0044	40.9	40.9
IPCA 2	13	8.571	0.659	1.946	0.0394	27.0	67.9
IPCA 3	11	7.036	0.640	1.888	0.0560	22.2	90.1
Residual	21	3.146	0.150	0.442	0.9806	9.9	100.0
Error	69	23.378	0.339				

† Abbreviations: AMMI = additive main effects and multiplicative interaction; GEI = genotype × environment interaction; IPCA = interaction principal component analysis axis.

ments with lower minimum heat indices. The heat index (apparent temperature) combines air temperature and relative humidity (Steadman, 1979). The minimum heat indices ranged from 21.84 to 24.16°C across environments, with a mean of 22.87°C. Locations were consistent across years as to whether their respective minimum heat indices were greater than or less than the mean minimum heat index. Locations with heat indices less than the mean minimum heat index were Ganado (22.56, 21.84, and 22.76°C for 2000, 2001, and 2002, respectively) and Beaumont (22.29, 22.15, and 21.93°C), while those with heat indices greater than the mean minimum heat index were Bay City (23.14, 23.19, and 22.99°C) and Eagle Lake (23.53, 23.86, and 24.16°C).

AMMI Biplot Analysis

The main and IPCA 1 effects of both G and E on grain yield were shown in Fig. 2. The AMMI biplot illustrates 84.2% of treatment SS (118.702), with 17.8% due to G SS (21.174), 55.4% due to E SS (65.795), and 10.9% due to IPCA 1 SS (12.980). Since IPCA 1 SS is 61.3% that of the G SS, this emphasizes the importance of taking GE interaction into consideration when estimating cultivar yield at different locations or when targeting rice cultivars onto specific locations.

For any G–E combination in the AMMI biplot (Fig. 2), the additive part (main effects) of the AMMI model equals the G mean plus the E mean minus the grand mean, and the multiplicative part (interaction effect) is the product of G and E IPCA 1 scores (Zobel et al., 1988). For example, Wells at Beaumont in 2002 had a main effect of $8.82 + 10.03 - 8.33 = 10.52$ kg ha^{-1}, and an interaction effect of $1.16 \times 0.40 = 0.46$ kg ha^{-1}. The AMMI model estimated the yield of Wells at Beaumont in 2002 as $10.52 + 0.46 = 10.98$ kg ha^{-1}, which fits the observed yield of 10.93 kg ha^{-1}. In comparison, the yield estimated by the ANOVA model was 10.52 kg ha^{-1}.

Rice cultivars that had IPCA 1 scores >0 responded

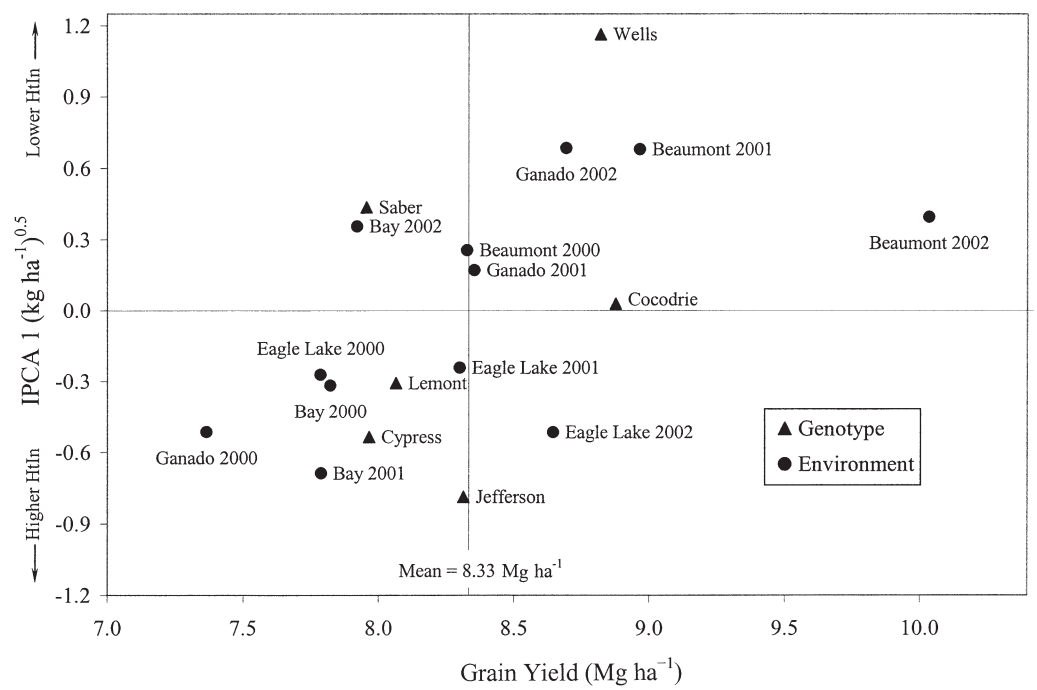

Fig. 2. AMMI biplot showing the main and IPCA 1 effects of both genotypes and environments on grain yield. IPCA 1 scores are in units equal to the square root of grain yield. An estimate of the GE interaction effect for a specific genotype–environment combination is the product of their corresponding IPCA 1 scores. Abbreviations: AMMI–Additive main effects and multiplicative interaction; IPCA–Interaction principal components analysis axis; HtIn–Heat index.

positively (adaptable) to environments that had IPCA 1 scores >0 (i.e., their interaction is positive) but responded negatively to environments that had IPCA 1 scores <0. The reverse applies for rice cultivars that had IPCA 1 scores <0. Hence, Cocodrie, Saber, and Wells were adapted to Bay City (2002), Ganado (2001 and 2002), and Beaumont (2000, 2001, and 2002). In contrast, Cypress, Jefferson and Lemont were adapted to Bay City (2000 and 2001), Ganado (2000) and Eagle Lake (2000, 2001, and 2002).

The differences among cultivars in terms of direction and magnitude along the *x* axis (yield) and *y* axis (IPCA 1 scores) were also important. The best cultivar should be high-yielding and stable across environments. For example, the two highest yielding cultivars, Cocodrie (8.88 Mg ha^{-1}) and Wells (8.82 Mg ha^{-1}), can be differentiated on the basis of their stability. The cultivar with a lower absolute IPCA 1 score (Cocodrie) would produce a lower absolute GE interaction effect than the cultivar with a higher absolute IPCA 1 score (Wells) and have a less variable (more stable) yield across environments. The cultivar stability ranking based on lower absolute IPCA 1 scores was Cocodrie (0.28), Lemont (0.307), Saber (0.437), Cypress (0.536), Jefferson (0.787), and Wells (1.164). Hence, Cocodrie was identified as the best cultivar (highest yield and stability).

Ganado had the highest variability in interaction (IPCA 1 scores) from year to year, while Eagle Lake had the least. This indicated that relative rankings of cultivars were more stable at Eagle Lake than at Ganado, making it difficult to recommend a specific cultivar for Ganado.

Targeting Rice Genotypes based on Nominal Yield

Estimates of cultivar nominal grain yields, on the basis of the AMMI model equation without the environmental deviation β_e (i.e., based on G and GE IPCA 1 effects only), across E ICPA 1 scores indicated the adaptability of each cultivar and aided in the identification of the cultivar that yielded the highest at specific E IPCA 1 ranges (Fig. 3). The biplot represents the combined SS of G (21.17) and IPCA 1 (12.98) or 64.6% of the G + GE SS (52.90). Cocodrie had the highest nominal grain yield at E IPCA 1 <0.049. Environments within this IPCA 1 score range were Bay (2000 and 2001), Eagle Lake (2000, 2001, and 2002), and Ganado (2000). Wells had the highest nominal grain yield at environments that had IPCA 1 scores >0.049. Environments within this IPCA 1 score range were Bay City (2002), Beaumont (2000, 2001, and 2002), and Ganado (2001 and 2002). On the basis of the frequency that a cultivar was expected to yield highest in a location, Wells should be recommended for both Ganado and Beaumont, while Cocodrie should be recommended for Eagle Lake and Bay City.

Since E IPCA 1 scores were negatively correlated with environment minimum heat indices, then Wells, which had the highest nominal yield at environments with IPCA 1 scores >0.049, would be adapted to environments with low minimum heat indices. Five of the six environments, which had IPCA 1 >0.049, had minimum heat indices that were less than the mean minimum heat index (averaged across environments, 22.87°C). Wells, which was produced from a Newbonnet/3/Lebonnet/

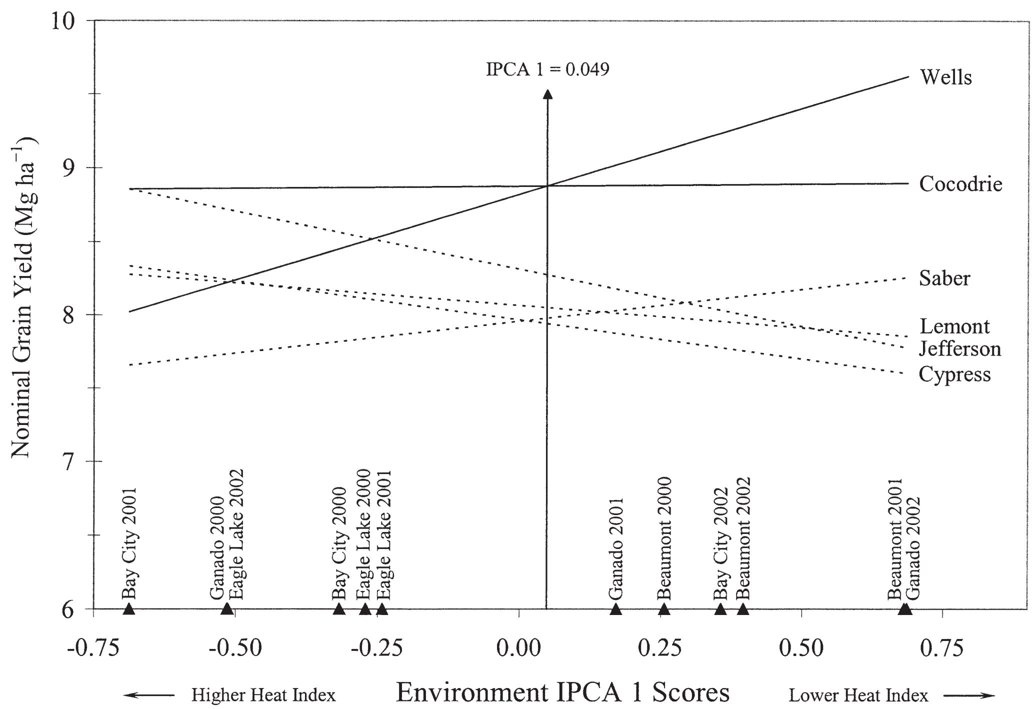

Fig. 3. Nominal grain yields of six rice cultivars, based on the AMMI model equation without environmental deviation, across environment IPCA 1 scores. Cocodrie was highest yielder at IPCA 1 <0.049, while Wells was highest yielder at IPCA 1 >0.049. Abbreviations: AMMI–Additive main effects and multiplicative interaction; IPCA–Interaction principal components analysis axis.

CI9902//Labele cross and released as a cultivar in Arkansas in 1989, is the current primary cultivar grown commercially in Arkansas (Evans, 2004) and Missouri (Beck, 2004), which have relatively lower temperatures than Texas. Cocodrie, on the other hand, had a stable nominal yield regardless of the environment's minimum heat index.

In addition to adaptability, the AMMI biplot (Fig. 3) showed the stability of a cultivar's nominal yield across environments. Cocodrie's nominal yield ranged from 8.86 to 8.90 Mg ha^{-1} across 12 environments. Because of its high and stable nominal yield across environments, Cocodrie was identified as the best cultivar among the six cultivars tested. Lemont also showed stability, with its nominal yield ranging from 7.85 to 8.28 Mg ha^{-1} across 12 environments. Lemont's moderately high yield and stable performance is one of the reasons why it was the most popular cultivar during the 1990s. Saber, which is a relatively new cultivar, had only moderate yield and stability.

The AMMI biplot can be used to identify the appropriate check cultivar for all locations (general check) or for specific locations (specific check). Rice breeders would then compare their promising lines against either the general or specific check cultivar in selecting for the next high yielding cultivar. For example, results from this study suggest that Cocodrie should be the general check cultivar for all environments because of its high and stable nominal yield across environments. In addition, Wells should be included in the MET and serve as an additional check cultivar at the Beaumont and Ganado test locations, since it had the highest nominal yield at these locations during three and 2 yr, respectively.

The AMMI biplot also sets the standard for nominal yield and stability levels that any upcoming rice cultivar should surpass. Rice breeders should aim for a cultivar with a stable yield performance (similar to that of Cocodrie), yet capable of out-yielding Wells and Cocodrie at the positive and negative ends of the E IPCA 1 scores, respectively.

SREG GGE Biplot Analysis

Performance of Different Genotypes at a Specific Environment

The GGE biplot of the SREG analysis results was used to show the relative performance of all cultivars at a specific environment. As an example, the 2002 Beaumont environment was used since it produced the highest yield among the 12 environments. A line was drawn that passed through the biplot's origin and the Bea02 (Beaumont, 2002) marker to make a Bea02 axis, and then a broken line was perpendicularly drawn from each cultivar toward the Bea02 axis (Fig. 4). The cultivars were ranked on the basis of their projections onto the Bea02 axis, with rank increasing in the direction toward the positive end (Yan et al., 2000; Yan and Hunt, 2002). In this example, the cultivar yield ranking at

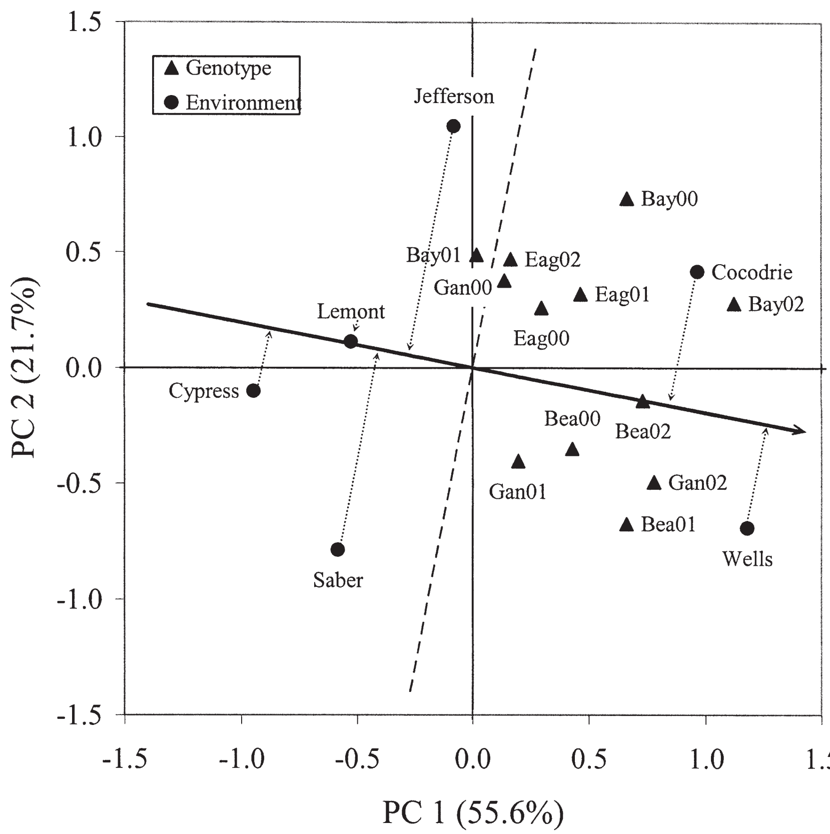

Fig. 4. Genotype plus genotype × environment (GGE) biplot obtained from sites regression (SREG) analysis showing the performance of different genotypes at Beaumont in 2002. Abbreviations: Bay–Bay City, Bea–Beaumont, Eag–Eagle Lake, Gan–Ganado, 00–2000, 01–2001, 02–2002.

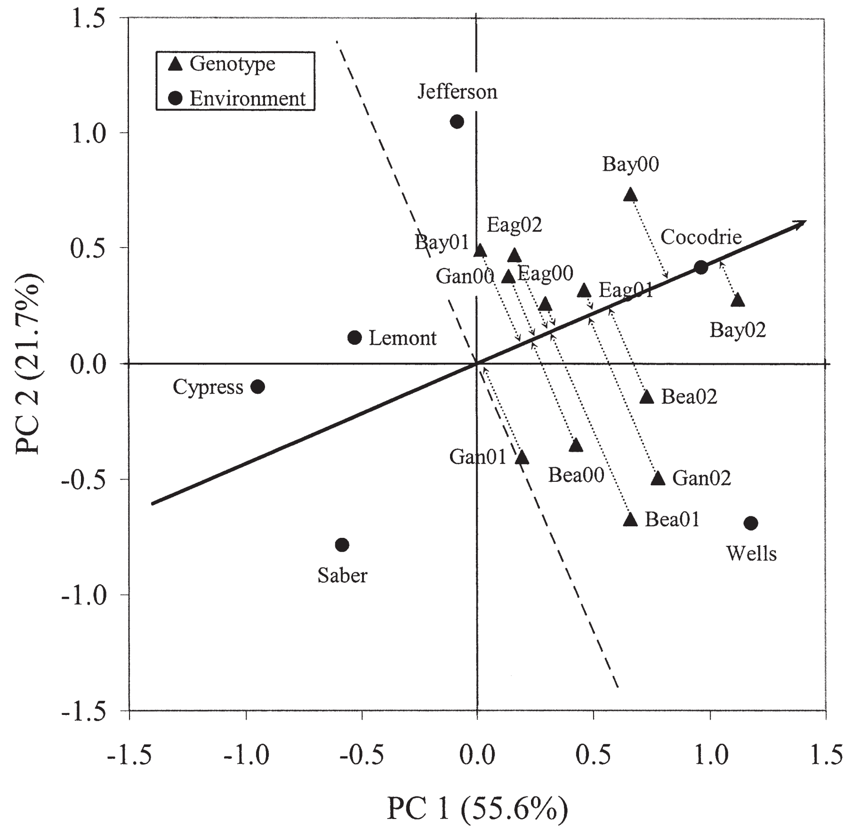

Fig. 5. Genotype plus genotype × environment (GGE) biplot obtained from sites regression (SREG) analysis showing the performance of Cocodrie at different environments. Abbreviations: Bay–Bay City, Bea–Beaumont, Eag–Eagle Lake, Gan–Ganado, 00–2000, 01–2001, 02–2002.

Beaumont in 2002 was as follows: Wells, Cocodrie, Jefferson, Saber, Lemont, and Cypress. The broken line, which passed through the plot's origin and was perpendicular to the 2002 Beaumont environment vector, separated the cultivars (Wells and Cocodrie) that had higher than average yield from cultivars (Jefferson, Saber, Lemont, and Cypress) that had lower than average yield.

Relative Adaptation of a Specific Genotype across Environments

The GGE biplot was used to show the relative performance of a specific cultivar at different environments. Cocodrie (the current primary grown at Texas) was used in this example (Fig. 5). A Cocodrie axis was made by drawing a line that passed through the biplot's origin and the Cocodrie marker, and then broken lines were drawn from each environment perpendicularly toward the Cocodrie axis. An environment's rank in producing Cocodrie grain yield was based on its projection onto the Cocodrie axis, with rank increasing in the direction toward the Cocodrie marker (Yan et al., 2000; Yan and Hunt, 2002). Hence, Cocodrie would yield highest at Bay City (2002), followed by Bay City (2000), Beaumont (2002), Eagle Lake (2001), Ganado (2002), Eagle Lake (2000), Beaumont (2001), Eagle Lake (2002), Ganado (2000), Beaumont (2000), Bay City (2001), and Ganado (2001). The broken line that passed through the biplot's origin and that was perpendicular to the Cocodrie axis separated the environments where Cocodrie would yield above-average and below-average.

Comparison of Two Genotypes in Different Environments

The performance of the top two grain yielding cultivars (Cocodrie and Wells) when considering only the G and GE interactions was compared by the GGE biplot (Fig. 6). A line that connected the markers of Cocodrie and Wells was drawn, and then a broken line that was perpendicular to the first line and that passed through the plot origin was drawn. The broken line separated the GGE coordinates into two groups, with each cultivar yielding better than the other within its respective side of the broken line. Thus, Cocodrie would yield better than Wells at seven environments (Bay City [2000, 2001, and 2002], Eagle Lake [2000, 2001, and 2002], and Ganado [2000]), while Wells would yield better than Cocodrie at five environments (Beaumont [2000, 2001, 2002], and Ganado [2001 and 2002]).

Identification of the Best Genotype for each Environment

The markers of cultivars that were farthest from the GGE biplot origin (Cypress, Jefferson, Cocodrie, Wells, and Saber) served as corners of a polygon when these markers were connected with straight lines, while the lines that started from the biplot origin and were perpendicular to the sides of the polygon delimited the five sectors formed (Fig. 7). Only three of the five sectors contained environments and these were identified as the three megaenvironments. The group of environ-

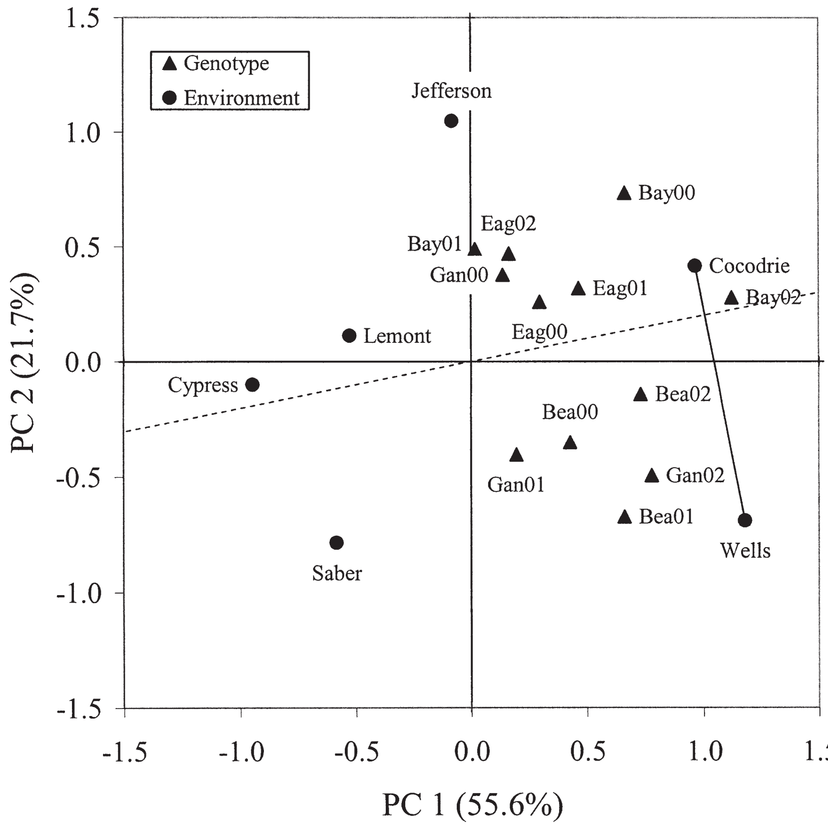

Fig. 6. Genotype plus genotype × environment (GGE) biplot obtained from sites regression (SREG) analysis that groups the environments into those where Cocodrie outyields Wells (above the broken line) and where Wells outyields Cocodrie (below the broken line). Abbreviations: Bay–Bay City, Bea–Beaumont, Eag–Eagle Lake, Gan–Ganado, 00–2000, 01–2001, 02–2002.

ments that share the same best cultivar(s) (identified as being located at the corner of the polygon) is termed the megaenvironment (Yan et al., 2000; Yan and Hunt, 2002). Hence, Jefferson was the highest yielding cultivar in the megaenvironment sector that consisted of Bay City (2001), Eagle Lake (2002) and Ganado (2000). Cocodrie was the highest yielding cultivar at the megaenvironment that consisted of Bay City (2000 and 2002) and Eagle Lake (2000 and 2001). Wells was the highest yielding cultivar at the megaenvironment that consisted of Beaumont (2000, 2001, and 2002), and Ganado (2001 and 2002). Cypress, Lemont, and Saber were low yielding cultivars at all environments, with Cypress and Saber being the two lowest yielding cultivars since they were located farthest from the environments.

Multilocation trials conducted across years are necessary to verify the pattern of locations grouped into megaenvironments and genotypes identified as highest grain yielders for each megaenvironment (Yan et al., 2000; Yan and Rajcan, 2002). A preferred genotype is one that consistently yields the highest at the same location(s) across years. At Bay City, Cocodrie was the highest yielder for 2 yr, while Jefferson was the highest yielder for 1 yr. Beaumont had Wells as its highest yielder for all 3 yr (Fig. 7). At Eagle Lake, Cocodrie was the highest yielder for 2 yr while Jefferson for 1 yr. Ganado had Wells as its highest yielder for 2 yr and Jefferson for 1 yr. Since megaenvironments are determined by the frequently highest yielding cultivars, then only two megaenvironments instead of three would remain. Bay City and Eagle Lake would comprise one megaenvironment with Cocodrie as its recommended cultivar, while Beaumont and Ganado would comprise another megaenvironment with Wells as its recommended cultivar.

Results from both AMMI and SREG GGE biplot analyses indicated that Cocodrie was the best cultivar in terms of better yield mostly at Bay City and Eagle Lake, while Wells was the best cultivar mostly at Beaumont and Ganado. Both analyses also indicate that Wells qualifies as a check cultivar in multilocation trials of promising lines conducted at Beaumont and Ganado.

Identification of Ideal Cultivar

The requirement for the use of SREG-based GGE biplots in the identification of superior cultivars and ideal test environments that facilitate the identification of such cultivars is a high correlation ($r > 0.95$) between G PC1 scores and G yields (averaged across locations) (Yan et al., 2000; Yan et al., 2001; Yan and Rajcan, 2002; Crossa et al., 2002). Ideal cultivars are those that should have large PC1 scores (high mean yield) and small (absolute) PC2 scores (high stability) (Yan et al., 2000; Yan and Rajcan, 2002). Yan and Hunt (2002) further suggested that a mean-environment coordinates system be created by drawing a mean-environment axis line that passes through the biplot origin and the mean

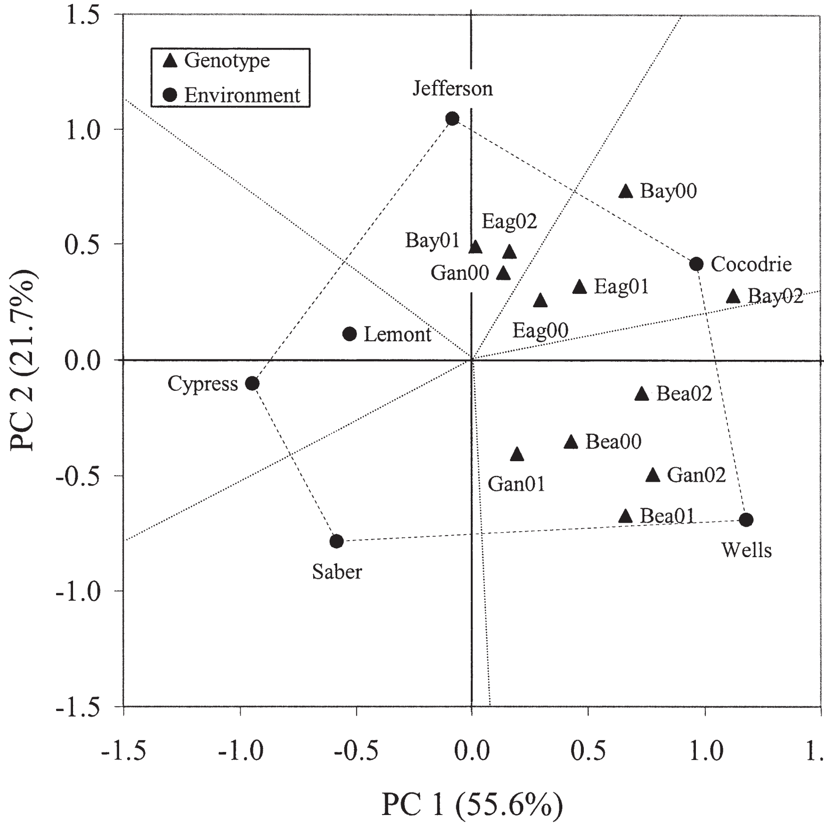

Fig. 7. Genotype plus genotype × environment (GGE) biplot obtained from sites regression (SREG) analysis showing the megaenvironments and their respective highest yielding cultivars. Abbreviations: Bay–Bay City, Bea–Beaumont, Eag–Eagle Lake, Gan–Ganado, 00–2000, 01–2001, 02–2002.

environment marker. In addition, a broken line that is perpendicular to the mean-environment axis and that passes through the biplot origin is drawn.

In this study, the correlation between cultivar PC1 scores and cultivar yields was high ($r = 0.983$). Hence, the G main effects can be represented by the cultivars PC1 scores. The yield ranking of cultivars relative to the positive end of the mean-environment axis was Wells, Cocodrie, Jefferson, Lemont, Saber, and then Cypress (Fig. 8). The stability ranking of cultivars based on increasing absolute difference between the genotype markers and the mean-environment axis was Cypress, Lemont, Cocodrie, Saber, Wells, and then Jefferson. Although Wells was the highest yielding cultivar, it was undesirably the fifth in stability, and although Cypress was first in stability, it was last in yielding ability. When both yield and stability rankings were considered, it was Cocodrie that had the second highest yield and third highest stability that qualified as the best among these six cultivars. The PC1 and PC2 scores obtained from SREG analysis that respectively represent the G yield and stability are respectively comparable to the G effect (yield) and adaptability parameter (regression coefficient, b) of Finlay and Wilkinson (1963).

Although both AMMI and SREG GGE biplot analyses identified Cocodrie as the best cultivar, their stability ranking results differed. This was probably due to the difference in the amount of GGE variation accounted for by each analysis. The AMMI analysis results (Fig. 2 and 3) accounted for 64.6% of GGE variation, while the SREG GGE biplot analysis results accounted for 77.3%.

Identification of Ideal Test Locations

Ideal test environments should have small (absolute) PC2 scores (more representative of the overall environment) and large PC1 scores (more power to discriminate genotypes in terms of the genotypic main effect) (Yan et al., 2000; Yan and Rajcan, 2002). The ranking of environments in terms of being the most representative environment (based on the absolute difference between environment markers and the mean-environment axis) was Bay City (2002), followed by Eagle Lake (2000, 2001), Beaumont (2002), Ganado (2000), and Beaumont (2000), Ganado (2001), Eagle Lake (2002), Bay City (2001), Ganado (2002), Bay City (2000), then Beaumont (2001). Eagle Lake had an average rank of 4.7, both Bay City and Beaumont had an average rank of 7, while Ganado had an average rank of 7.3. Selection during segregating generations or during trials that do not require testing across several locations are usually performed at one location that best represents the region where the newly developed cultivar is going to be recommended for production. Eagle Lake was the location identified as the most representative among the four locations tested.

The ranking of environments in terms of their ability to discriminate cultivars (based on the relative position

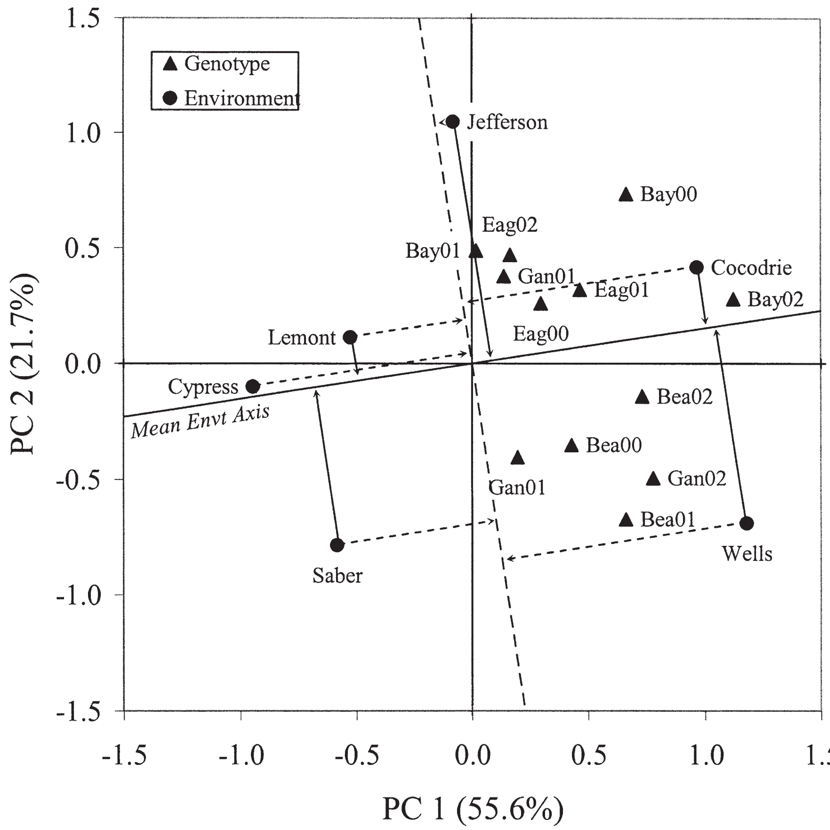

Fig. 8. Genotype plus genotype × environment (GGE) biplot obtained from sites regression (SREG) analysis showing the yielding ability (higher yielding cultivars have their solid lines located toward the positive end of the mean environment axis) and stability (more stable lines have their broken lines nearer to the mean-environment axis) of six rice genotypes. The percentage of GGE variation accounted for by each PC axis is also shown. Abbreviations: Bay–Bay City, Bea–Beaumont, Eag–Eagle Lake, Gan–Ganado, 00–2000, 01–2001, 02–2002.

of each environment's marker to the positive end of the mean-environment axis) was Bay City (2002 and 2000), Beaumont (2002), Ganado (2002), Beaumont (2001), Eagle Lake (2001), Beaumont (2000), Eagle Lake (2000 and 2002), Ganado (2000 and 2001), and Bay City (2001). Both Bay City and Beaumont had an average rank of 5.0, Eagle Lake had an average rank of 7.7, and Ganado had an average rank of 8.3. Selection trials that require testing across several locations, such as the advanced yield trials require locations that can discriminate and determine the differences in the performance of the rice genotypes being tested. This is required in order that the best cultivar for the whole region or for specific sub-regions can be identified and recommended. Both Bay City and Beaumont were identified as the locations that had better genotype-discriminating abilities than the other locations.

SUMMARY

This paper demonstrated the usefulness of AMMI model, SREG model, and GGE biplot analyses in the interpretation of grain yield data from a multienvironment experiment. The AMMI model analysis provided estimates of the magnitude and significance of the effects of GE interaction and its interaction principal components relative to G and E effects. Stability and adaptability of genotypes were estimated though AMMI biplots. Estimates of genotype nominal grain yield at different environments aided in the identification of the genotype that yielded the highest at specific E IPCA 1 ranges or megaenvironments, and in the identification of the appropriate check cultivar for all locations or for specific locations. Furthermore, locations that have stable genotype yield rankings across years were identified.

The GGE biplots of SREG analysis results were used to determine the relative performance of genotypes at a specific environment, compare the performance of a genotype at different environments, compare the performance of two genotypes at different environments, identify the highest yielding genotypes at the different megaenvironments, and identify ideal cultivars and test locations.

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